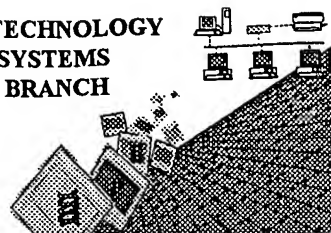# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _/0/0/9,1/4_

Source: _PCT/0_

Date Processed by STIC: _4/2/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN ASSISTANCE: e-mail: robert.wax @ uspto.gov Telephone: 703-306-4119

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
   EFFECTIVE MAY 1, 2003 (via USPS): Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
       Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/01/2003

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/019,114_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering
The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/019,114**

DATE: 04/02/2003
TIME: 12:50:31

Input Set : **A:\01997.013000 sequence listing.txt**
Output Set: **N:\CRF4\04022003\J019114.raw**

```
   5 <110> APPLICANT: Sagami Chemical Research Center,
   7        Protegene Inc.
  11 <120> TITLE OF INVENTION: Human proteins having hydrophobic domains and DNAs encoding
these
  13        proteins
  16 <130> FILE REFERENCE: 661925
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/019,114
C--> 20 <141> CURRENT FILING DATE: 2002-10-24
  20 <150> PRIOR APPLICATION NUMBER: JP 11-188835
  22 <151> PRIOR FILING DATE: 1999-07-02
  26 <160> NUMBER OF SEQ ID NOS: 30
```

many errors

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
  30 <210> SEQ ID NO: 1
  32 <211> LENGTH: 233
  34 <212> TYPE: PRT
  36 <213> ORGANISM: Homo sapiens
  40 <400> SEQUENCE: 1
  42 Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu Leu Leu Gly Ser
  44   1             5                  10                 15
  46 Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn
  48             20                  25                 30
  50 Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu
  52           35                  40                 45
  54 Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile
  56       50                  55                 60
  58 Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val
  60   65                  70                  75                 80
  62 Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn
  64               85                  90                  95
  66 Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp
E--> 68              100 100              105 105             110
  70 Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
  72           115                 120                 125
  74 Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
  76       130                 135                 140
  78 Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
  80 145                 150                 155                 160
  82 Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
  84               165                 170                 175
  86 Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
  88           180                 185                 190
```

misaligned number - see item 3 in Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 04/02/2003
PATENT APPLICATION: US/10/019,114   TIME: 12:50:31

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
 90 Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
 92         195             200             205          ·
 94 Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
 96         210             215             220
 98 Cys Asp Phe Pro Ser Phe Asn Leu Lys
100 225             230
103 <210> SEQ ID NO: 2
105 <211> LENGTH: 273
107 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 2
115 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
117   1             5                 10              15
119 Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
121             20              25              30
123 Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
125         35              40              45
127 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
E--> 129     50          ·     55              60
131 Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
E--> 133 65              70              75              80
135 Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
E--> 137             85              90              95
139 Gly Leu Pro Gly Ala Cys·Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
E--> 141             100             105             110
143 Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
E--> 145         115             120             125
147 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
E--> 149     130             135             140
151 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
E--> 153 145             150             155             160
155 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
E--> 157             165             170             175
159 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
E--> 161             180             185             190
163 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
E--> 165         195             200             205
167 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
E--> 169     210             215             220
171 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
E--> 173 225             230             235             240
175 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu·Ser Glu Gln
E--> 177             245             250             255
179 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
E--> 181             260             265             270
183 Ser
185 <210> SEQ ID NO: 3
187 <211> LENGTH: 282
189 <212> TYPE: PRT
```

Same misalignment errors (handwritten annotation)

P.3 (handwritten annotation)

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
191 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 3
197 Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu      same
199  1           5                  10                  15
201 Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro
203             20                  25                  30
205 Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu
207             35                  40                  45
209 Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr
211      50                  55                  60
213 Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
215  65                  70                  75                  80
217 Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
219                  85                  90                  95
221 Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala
223             100                 105                 110
225 Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys
227             115                 120                 125
229 Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr Cys Lys
231      130                 135                 140
233 Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys Glu Asn
235 145                 150                 155                 160
237 Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe Ile Ile
239                 165                 170                 175
241 Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln Ile Thr
243             180                 185                 190
245 Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile Gly Ser
247             195                 200                 205
249 Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala Pro Leu
251      210                 215                 220
253 Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val Val Ile
255 225                 230                 235                 240
257 Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro Asp Asp
259                 245                 250                 255
261 Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn His Lys
263             260                 265                 270
265 Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn
267      275                 280
270 <210> SEQ ID NO: 4
272 <211> LENGTH: 238
274 <212> TYPE: PRT                          P.4
276 <213> ORGANISM: Homo sapiens
280 <400> SEQUENCE: 4
282 Met Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu
284  1           5                  10                  15
286 Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
288             20                  25                  30
290 Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
292             35                  40                  45
```

```
      294 Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr
      296      50              55                  60
      298 Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
E--> 300  65          70                  75                  80
      302 Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
E--> 304              85                  90                  95
      306 Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
E--> 308             100                 105                 110
      310 Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
E--> 312         115                 120                 125
      314 Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
E--> 316         130                 135                 140
      318 Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn
E--> 320 145                 150                 155                 160
      322 Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
E--> 324             165                 170                 175
      326 Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val
E--> 328             180                 185                 190
      330 His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
E--> 332         195                 200                 205
      334 Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
E--> 336         210                 215                 220
      338 His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
E--> 340 225                 230                 235
      344 <210> SEQ ID NO: 5
      346 <211> LENGTH: 372
      348 <212> TYPE: PRT
      350 <213> ORGANISM: Homo sapiens
      354 <400> SEQUENCE: 5
      356 Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro
      358  1               5                   10                  15
      360 Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val
      362             20                  25                  30
      364 Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
      366             35                  40                  45
      368 Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
      370      50                  55                  60
      372 Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
E--> 374  65              70                  75                  80
      376 Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr
E--> 378             85                  90                  95
      380 Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu
E--> 382             100                 105                 110
      384 Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg
E--> 386             115                 120                 125
      388 Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly
E--> 390             130                 135                 140
      392 Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His
E--> 394 145                 150                 155                 160
```

same

same

file://C:\CRF4\Outhold\VsrJ019114.htm   4/2/03

RAW SEQUENCE LISTING   DATE: 04/02/2003
PATENT APPLICATION: US/10/019,114 TIME: 12:50:31

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
      396 Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe
E--> 398                 165             170             175
      400 Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val
E--> 402         180             185             190
      404 Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val
E--> 406         195             200             205
      408 Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr
E--> 410     210             215             220
      412 Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu
E--> 414 225             230             235             240
      416 Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val
E--> 418             245             250             255
      420 Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
E--> 422         260             265             270
      424 Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
E--> 426         275             280             285
      428 Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
E--> 430     290             295             300
      432 Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
E--> 434 305             310             315             320
      436 Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
E--> 438             325             330             335
      440 Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
E--> 442         340             345             350
      444 Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
E--> 446     355             360             365
      448 Asp Ser Ala Leu
E--> 450     370
      454 <210> SEQ ID NO: 6
      456 <211> LENGTH: 146
      458 <212> TYPE: PRT
      460 <213> ORGANISM: Homo sapiens
      464 <400> SEQUENCE: 6
      466 Met Trp Lys Leu Trp Arg Ala Glu Glu Gly Ala Ala Ala Leu Gly Gly
      468   1             5             10             15
      470 Ala Leu Phe Leu Leu Leu Phe Ala Leu Gly Val Arg Gln Leu Leu Lys
      472             20             25             30
      474 Gln Arg Arg Pro Met Gly Phe Pro Pro Gly Pro Pro Gly Leu Pro Phe
      476         35             40             45
      478 Ile Gly Asn Ile Tyr Ser Leu Ala Ala Ser Ser Glu Leu Pro His Val
      480     50             55             60
      482 Tyr Met Arg Lys Gln Ser Gln Val Tyr Gly Glu Val Gln Pro Arg Arg
      484  65             70             75             80
      486 Ala Pro Gly Arg Glu Gly Arg Gln Ala Gly Pro Gly Trp Pro Gly Pro
      488             85             90             95
      490 Ser Trp Leu Asp Leu Trp Pro Pro Leu Gly Arg Leu Val Gly Thr Ser
E--> 492         100             105             110
      494 Pro Cys Ala Gly Cys Pro Leu Arg Asp Thr Arg Phe Pro Gly Leu Glu
E--> 497     115             120             125
```

same

same

P. 6

```
      499 Gly Arg Ser Pro Arg Arg Arg Ala Pro Leu Gln Gly Glu Pro Arg Pro
E--> 501     130             135                 140
      503 Cys Arg
      505 145
      508 <210> SEQ ID NO: 7
      510 <211> LENGTH: 302
      512 <212> TYPE: PRT
      514 <213> ORGANISM: Homo sapiens
      518 <400> SEQUENCE: 7
      520 Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
      522   1               5               10                  15
      524 Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu
      526             20              25                  30
      528 Cys Leu Ala Thr Cys Leu Asp His His Phe Pro Thr Gly Ser Arg Pro
      530             35              40                  45
      532 Thr Val Pro Gly Pro Leu His Phe Ser Gly Tyr Ser Ser Val Pro Asp
      534         50              55                  60
      536 Gly Lys Pro Leu Val Arg Glu Pro Cys Arg Ser Cys Ala Val Val Ser
      538  65                 70                  75                  80
      540 Ser Ser Gly Gln Met Leu Gly Ser Gly Leu Gly Ala Glu Ile Asp Ser
      542                 85              90                  95
      544 Ala Glu Cys Val Phe Arg Met Asn Gln Ala Pro Thr Val Gly Phe Glu
      546             100             105                 110
      548 Ala Asp Val Gly Gln Arg Ser Thr Leu Arg Val Val Ser His Thr Ser
      550         115             120                 125
      552 Val Pro Leu Leu Leu Arg Asn Tyr Ser His Tyr Phe Gln Lys Ala Arg
      554         130             135                 140
      556 Asp Thr Leu Tyr Met Val Trp Gly Gln Gly Arg His Met Asp Arg Val
      558 145             150                 155                 160
      560 Leu Gly Gly Arg Thr Tyr Arg Thr Leu Leu Gln Leu Thr Arg Met Tyr
E--> 562             165             170                 175
      564 Pro Gly Leu Gln Val Tyr Thr Phe Thr Glu Arg Met Met Ala Tyr Cys
E--> 566             180             185                 190
      568 Asp Gln Ile Phe Gln Asp Glu Thr Gly Lys Asn Arg Arg Gln Ser Gly
E--> 570         195             200                 205
      572 Ser Phe Leu Ser Thr Gly Trp Phe Thr Met Ile Leu Ala Leu Glu Leu
E--> 574         210             215                 220
      576 Cys Glu Glu Ile Val Val Tyr Gly Met Val Ser Asp Ser Tyr Cys Arg
E--> 578 225             230                 235                 240
      580 Glu Lys Ser His Pro Ser Val Pro Tyr His Tyr Phe Glu Lys Gly Arg
E--> 582             245             250                 255
      584 Leu Asp Glu Cys Gln Met Tyr Leu Ala His Glu Gln Ala Pro Arg Ser
E--> 586             260             265                 270
      588 Ala His Arg Phe Ile Thr Glu Lys Ala Val Phe Ser Arg Trp Ala Lys
E--> 590             275             280                 285
      592 Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp Arg Thr Glu
E--> 594         290             295                 300
      661 <210> SEQ ID NO: 9
      663 <211> LENGTH: 542
```

same

same

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,114

DATE: 04/02/2003
TIME: 12:50:31

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
665 <212> TYPE: PRT
667 <213> ORGANISM: Homo sapiens
671 <400> SEQUENCE: 9
673 Met Lys Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe
675   1               5                  10                  15
677 Leu Ser Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser
679               20                  25                  30
681 Tyr Ser Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn
683               35                  40                  45
685 Trp Ala Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser
687       50                  55                  60
689 Val Asn Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn
691   65                  70                  75                  80
693 Ile Val Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His
695                   85                  90                  95
697 Asn Thr Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr
699   .               100                 105                 110
701 Thr Glu Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg
703               115                 120                 125
705 Lys Leu Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr
707       130                 135                 140
709 Leu Gly Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro
711 145                 150                 155                 160
713 Arg Gln Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu
715                   165                 170                 175
717 Gln Glu Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala
E--> 719           180                 185                 190
721 Arg Ala Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu
E--> 723           195                 200                 205
725 Lys Ala Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg
E--> 727       210                 215                 220
729 Cys Asn Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser
E--> 731 225                 230                 235                 240
733 Lys Ser Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu
E--> 735           245                 250                 255
737 Ser Val Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr
E--> 739           260                 265                 270
741 Val Trp Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val
E--> 743           275                 280                 285
745 Cys Ile Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe
E--> 747       290                 295                 300
749 Ile Ile Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys
E--> 751 305                 310                 315                 320
753 Val Ala Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe
E--> 755               325                 330                 335
757 Trp Met Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile
E--> 759           340                 345                 350
761 Phe Arg Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile
E--> 763           355                 360                 365
```

same

P.8

RAW SEQUENCE LISTING   DATE: 04/02/2003
PATENT APPLICATION: US/10/019,114   TIME: 12:50:31

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
       765 Gly Tyr Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr
E--> 767     370                 375                 380
       769 Glu Pro Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp
E--> 771 385                 390                 395                 400
       773 Asp Asn Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile
E--> 775                 405                 410                 415
       777 Val Ala Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln
E--> 779                 420                 425                 430
       781 Arg Pro Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met
E--> 783                 435                 440                 445
       785 Arg Ile Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr
E--> 787     450                 455                 460
       789 Trp Gly Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe
E--> 791 465                 470     475                         480
       793 His Ile Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu
E--> 795                 485                 490                 495
       797 Leu Phe Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met
E--> 799                 500                 505                 510
       801 Arg Met Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser
E--> 803         515                 520                 525
       805 Leu Gly Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly
E--> 807     530                 535                 540
```

811 <210> SEQ ID NO: 10
813 <211> LENGTH: 276
815 <212> TYPE: PRT
817 <213> ORGANISM: Homo sapiens
821 <400> SEQUENCE: 10

```
       823 Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
       825   1                 5                 10                15
       827 Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
       829                 20                 25                 30
       831 Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
       833                 35                 40                 45
       835 Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala
       837      50                 55                 60
       839 Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
       841  65                 70                 75                 80
       843 Arg Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro
       845                 85                 90                 95
       847 Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
       849                 100                105                110
       851 Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
       853         115                 120                125
       855 Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
       857     130                 135                 140
       859 Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met
       861 145                 150                 155                160
       863 Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile
       865                 165                 170                175
```

Input Set : A:\01997.013000 sequence listing.txt
Output Set: N:\CRF4\04022003\J019114.raw

```
          867 Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly
          869             180             185             190
          871 Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu
          873         195             200             205
          875 Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe
          877     210             215             220
          879 Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly
          881 225             230             235             240
          883 Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu
E-->      885             245             250             255
          887 Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro
E-->      889             260             265             270
          891 Ser Leu Ser Pro
          893         275
         1324 <210> SEQ ID NO: 21
         1326 <211> LENGTH: 1308
         1328 <212> TYPE: DNA
         1330 <213> ORGANISM: Homo sapiens
         1334 <220> FEATURE:
         1336 <221> NAME/KEY: CDS
         1338 <222> LOCATION: (76)...(777)
         1341 <400> SEQUENCE: 21
         1343 aaagaattcg aaaccgactt gcagaagtta aatgcccttg gaaagggact gctattttat   60
         1345 taaggcagat cccaa atg tgg cag ctt tta gca gca gca tgc tgg atg ctt  111
         1347                  Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu
         1349                   1               5               10
         1351 ctt ctt gga tct atg tat ggt tat gac aag aaa gga aac aat gca aac  159
         1353 Leu Leu Gly Ser Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn
         1355         15              20              25
E-->     1357 cct gaa gct aat atg aat att agc cag att att tct tac tgg ggt tat  207
         1359 Pro Glu Ala Asn Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr
         1361     30              35              40
         1363 cct tat gaa gag tat gat gtt aca aca aaa gat ggt tat atc ctt gga  255
         1365 Pro Tyr Glu Glu Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly
         1367  45              50              55              60
         1369 att tat agg att cca cat gga aga gga tgc cca ggg agg aca gct cca  303
         1371 Ile Tyr Arg Ile Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro
         1373             65              70              75
         1375 aag cct gct gtg tat ttg cag cat ggc tta att gca tct gcc agt aac  351
         1377 Lys Pro Ala Val Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn
         1379         80              85              90
         1380 tgg att tgc aac ctg ccc aac aac agt ttg gct ttc ctt ctg gca gat  399
         1382 Trp Ile Cys Asn Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp
W-->     1384         95              100             105
         1386 agt ggt tat gac gtg tgg ttg ggg aac agc cga gga aac act tgg tcc  447
         1388 Ser Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser
W-->     1390         110             115             120
         1392 aga aaa cac ctt aaa ttg tca ccg aaa tca cca gaa tac tgg gcc ttc  495
         1394 Arg Lys His Leu Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe
```

(handwritten annotations: "same" near line 887; "Φ invalid nucleotide" near line 1355; "misaligned hos." near lines 1384–1390)

```
W--> 1396 125                  130                 135                  140
     1398 agt ttg gat gag atg gct aaa tat gac ctt cca gcc aca atc aat ttt      543
     1400 Ser Leu Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe
W--> 1402                145                 150                 155
     1404 atc ata gag aaa act gga cag aag cga ctc tac tac gtg ggc cac tca      591
     1406 Ile Ile Glu Lys Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser
W--> 1408                160                 165                 170
     1410 caa ggc acc acc ata gct ttt ata gca ttt tct aca aac cca gaa ctg      639
     1412 Gln Gly Thr Thr Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu
W--> 1414           175                 180                 185
     1416 gct aaa aag att aag ata ttt ttt gca ctg gct cca gtt gtc aca gtt      687
     1418 Ala Lys Lys Ile Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val
W--> 1420      190                 195                 200
     1422 aaa tac acc caa agt cct atg aaa aaa cta aca acc ctt tcc agg cga      735
     1424 Lys Tyr Thr Gln Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg
W--> 1426 205                 210                 215                  220
     1428 gta gtt aag gta tgt gac ttc cca agt ttt aat ctg aaa taacta          780
     1430 Val Val Lys Val Cys Asp Phe Pro Ser Phe Asn Leu Lys
W--> 1432                225                 230
     1434 aaagtagctc tatttccatt gatttcaaca gaagaccaat gacattttac aaacttctga    840
     1436 gaaaataata ggtattcaag atatccatgt aagttcactg atgatgtatg caatcttatt    900
     1438 agcagagttc agggaactcc ccctgttgct aatctgccct actttcttca tctatgtcta    960
     1440 gaaacgtgtc tgctgcgcca ttcctcaacc acagatagag agaacttatt tgattgattg   1020
     1442 gtttgttgaa tttagtagat tgaatttttc tagtgatccc taatttttta ggggcagtgg   1080
     1444 tggttgagtt cacagcatgg aatcagatgg tgtgtgtttg aatgttattt ctatgatttg   1140
     1446 caagctgggt aaatttggtc aagaccttaa gttctcttca tctgtaatgt ggggataata   1200
     1448 atagttctta ctcatagggc taccctgagg actaagtaaa ttaatacagc atatcctcta   1260
     1450 aaacaatgta ttgcatattg taaacctttta ataaatgtta acaattgt              1308
     1765 <210> SEQ ID NO: 24
     1767 <211> LENGTH: 1260
     1769 <212> TYPE: DNA
     1771 <213> ORGANISM: Homo sapiens
     1775 <220> FEATURE:
     1777 <221> NAME/KEY: CDS
     1779 <222> LOCATION: (147)...(863)
     1783 <400> SEQUENCE: 24
     1785 agcttccccc aagcggcggc agcaccacca gcggcagccg ccggagccgc cgccgcagcg     60
     1787 gggacgggga gccccggggg gccccgccac tgccgccgtc cgccgtcacc tacccggact    120
     1789 ggatcggcca gagttactcc gaggtg atg agc ctc aac gag cac tcc atg         170
     1791                                 Met Ser Leu Asn Glu His Ser Met
     1793                                   1               5
     1795 cag gcg ctg tcc tgg cgc aag ctc tac ttg agc cgc gcc aag ctt aaa     218
     1797 Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala Lys Leu Lys
     1799      10                  15                  20
     1801 gcc tcc agc cgg acc tcg gct ctg ctc tcc ggc ttc gcc atg gtg gca     266
     1803 Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala Met Val Ala
     1805 25                  30                  35                   40
     1807 atg gtg gag gtg cag ctg gac gct gac cac gac tac cca ccg ggg ctg     314
     1809 Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro Pro Gly Leu
```

687 same
↓
same
misaligned,
amino acid
nos.
in Seq. 22

P. 11

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,114

DATE: 04/02/2003

TIME: 12:50:31

Input Set : A:\01997.013000 sequence listing.txt

Output Set: N:\CRF4\04022003\J019114.raw

```
      1811                    45                    50                    55
      1813 ctc atc gcc ttc agt gcc tgc acc aca gtg ctg gtg gct gtg cac ctg    362
      1815 Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala Val His Leu
W--> 1817                    60                    65                    70
      1819 ttt gcg ctc atg atc agc acc tgc atc ctg ccc aac atc gag gcg gtg    410
      1821 Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile Glu Ala Val
W--> 1823          75                    80                    85
      1825 agc aac gtg cac aat ctc aac tcg gtc aag gag tcc ccc cat gag cgc    458
      1827 Ser Asn Val His Asn Leu Asn Ser Val Lys Glu Ser Pro His Glu Arg
W--> 1829          90                    95                   100
      1831 atg cac cgc cac atc gag ctg gcc tgg gcc ttc tcc acc gtc atc ggc    506
      1833 Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val Ile Gly
W--> 1835 105                   110                   115                   120
      1837 acg ctg ctc ttc cta gct gag gtg gtg ctg ctc tgc tgg gtc aag ttc    554
      1839 Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val Lys Phe
W--> 1841                   125                   130                   135
      1843 ttg ccc ctc aag aag cag cca ggc cag cca agg ccc acc agc aag ccc    602
      1845 Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser Lys Pro
W--> 1847                   140                   145                   150
      1849 ccc gcc agt ggc gca gca gcc aac gtc agc acc agc ggc atc acc ccg    650
      1851 Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile Thr Pro
W--> 1853          155                   160                   165
E--> 1855 ggc cag gca gct gcc atc gcc tcg acc acc atc atg gtg ccc ttc ggc    698
      1857 Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro Phe Gly
W--> 1859                   170                   175                   180
      1861 ctg atc ttt atc gtc ttc gcc gtc cac ttc tac cgc tca ctg gtt agc    746
      1863 Leu Ile Phe Ile Val Phe Ala Val His Phe Tyr Arg Ser Leu Val Ser
W--> 1865 185                   190                   195                   200
      1867 cat aag acc gac cga cag ttc cag gag ctc aac gag ctg gcg gag ttt    794
      1869 His Lys Thr Asp Arg Gln Phe Gln Glu Leu Asn Glu Leu Ala Glu Phe
W--> 1871                   205                   210                   215
      1873 gcc cgc tta cag gac cag ctg gac cac aga ggg gac cac ccc ctg acg    842
      1875 Ala Arg Leu Gln Asp Gln Leu Asp His Arg Gly Asp His Pro Leu Thr
W--> 1877                   220                   225                   230
      1879 ccc ggc agc cac tat gcc taggcccatg tggtctgggc ccttccagtg    890
      1881 Pro Gly Ser His Tyr Ala
W--> 1883          235
      1885 ctttggcctt acgcccttcc ccttgacctt gtcctgcccc agcctcacgg acagcctgcg    950
      1887 caggggctg ggcttcagca aggggcagag cgtggaggga agaggatttt tataagagaa   1010
      1889 atttctgcac tttgaaactg tcctctaaga gaataagcat ttcctgttct tccagctcca   1070
      1891 ggtccacctc ctgttgggag gcggtggggg gccaaagtgg ggccacacac tcgctgtgtc   1130
      1893 ccctctcctc ccctgtgcca gtgccacctg ggtgcctcct cctgtcctgt ccgtctcaac   1190
      1895 ctccctcccg tccagcattg agtgtgtaca tgtgtgtgtg acacataaat atactcataa   1250
      1897 ggacacctcc   1260
      1901 <210> SEQ ID NO: 25
      1903 <211> LENGTH: 1720
      1905 <212> TYPE: DNA
      1907 <213> ORGANISM: Homo sapiens
      1911 <220> FEATURE:
```

```
1913 <221> NAME/KEY: CDS
1915 <222> LOCATION: (282)...(1400)
1918 <400> SEQUENCE: 25
1920 agcaaagagc agtgcccagc ccagctcaga gggcaaatgg gacagatccc agaggccctg      60
1922 aggaggtctc tgctgctgat gaagctgtga ccaaacgcac ccaacccttg gcagccatct     120
1924 gtccctgcag ccatagccca cattcccatg acctccctct gcttgttttg ggaccatgtc     180
1926 tgtacagcct ctaggcccca gccccggagg tgaatgccat gccatgattc tggtgtgctc     240
1928 catggcatcc ccagcctagc tcccaatccc actttggcac g atg tta gcc aac         293
1930                                              Met Leu Ala Asn
1932                                               1
1934 agc tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct      341
1936 Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro Asp Tyr Arg Pro
1938   5                   10                  15                  20
1940 acc cac cgc ctg cac ttg gtg gtc tac agc ttg gtg ctg gct gcc ggg      389
1942 Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val Leu Ala Ala Gly
1944                   25                  30                  35
1946 ctc ccc ctc aac gcg cta gcc ctc tgg gtc ttc ctg cgc gcg ctg cgc      437
1948 Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu Arg Ala Leu Arg
1950                   40                  45                  50
```

E-->
```
1952 gtg cac tcg gtg gtg agc gtg tac atg tgt aac ctg gcg gcc age gac      485
1954 Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu Ala Ala Ser Asp
1956             55                  60                  65
```
(handwritten: invalid, arrow)

```
1958 ctg ctc ttc acc ctc tcg ctg ccc gtt cgt ctc tcc tac tac gca ctg      533
1960 Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser Tyr Tyr Ala Leu
1962             70                  75                  80
1964 cac cac tgg ccc ttc ccc gac ctc ctg tgc cag acg acg ggc gcc atc      581
1966 His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr Thr Gly Ala Ile
1968  85                  90                  95                 100
1970 ttc cag atg aac atg tac ggc agc tgc atc ttc ctg atg ctc atc aac      629
1972 Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu Met Leu Ile Asn
1974                  105                 110                 115
1976 gtg gac cgc tac gcc gcc atc gtg cac ccg ctg cga ctg cgc cac ctg      677
1978 Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg Leu Arg His Leu
1980                  120                 125                 130
1982 cgg cgg ccc cgc gtg gcg cgg ctg ctc tgc ctg ggc gtg tgg gcg ctc      725
1984 Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly Val Trp Ala Leu
1986                  135                 140                 145
1988 atc ctg gtg ttt gcc gtg ccc gcc gcc cgc gtg cac agg ccc tcg cgt      773
1990 Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His Arg Pro Ser Arg
1992                  150                 155                 160
1994 tgc cgc tac cgg gac ctc gag gtg cgc cta tgc ttc gag agc ttc agc      821
1996 Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe Glu Ser Phe Ser
1998 165                  170                 175                 180
2000 gac gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag      869
2002 Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu
2004                  185                 190                 195
2006 gcg ctg ggc ttc ctg ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc      917
2008 Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly
2010                  200                 205                 210
```

(handwritten: P.13)

```
       2012 cga gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg        965
       2014 Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg
       2016         215                 220                 225
       2018 cgg cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg       1013
       2020 Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu
       2022         230                 235                 240
       2024 ctg tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg       1061
       2026 Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val Tyr Gly Leu Leu
       2028 245                 250                 255                 260
       2030 cgg agc aag ctg gtg gcg gcc agc gtg cct gcc cgc gat cgc gtg cgc       1109
       2032 Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg
       2034                 265                 270                 275
       2036 ggg gtg ctg atg gtg atg gtg ctg ctg gcc ggc gcc aac tgc gtg ctg  ′.   1157
       2038 Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu
       2040                 280                 285                 290
E-->   2042 gac ccg ctg gtg tac tac ttt agc gcc gag ggc ttc cgc aac acc ctg       1205
       2044 Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe Arg Asn Thr Leu
       2046         295                 300                 305
       2048 cgc ggc ctg ggc act ccg cac cgg gcc agg acc tcg gcc acc aac ggg       1253
       2050 Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly
       2052         310                 315                 320
       2054 acg cgg gcg gcg ctc gcg caa tcc gaa agg tcc gcc gtc acc acc gac       1301
       2056 Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala Val Thr Thr Asp
       2058 325                 330                 335                 340
       2060 gcc acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac       1349
       2062 Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp
       2064                 345                 350                 355
       2066 tcc cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc       1397
       2068 Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu
       2070                 360                 365                 370
       2072 tga acacacatgc cattgcgctg tccgtgcccg actcccaacg cctctcgttc           1450
       2074 tgggaggctt acagggtgta cacacaagaa ggtgggctgg gcacttggac ctttgggtgg     1510
       2076 caattccagc ttagcaacgc agaagagtac aaagtgtgga agccagggcc cagggaaggc     1570
       2078 agtgctgctg gaaatggctt ctttaaactg tgagcacgca gagcacccct tctccagcgg     1630
       2080 tgggaagtga tgcagagagc ccacccgtgc agagggcaga agaggacgaa atgcctttgg     1690
       2082 gtgggcaggg cattaaactg ctaaaagctg                                      1720
       2503 <210> SEQ ID NO: 29
       2505 <211> LENGTH: 2667
       2507 <212> TYPE: DNA
       2509 <213> ORGANISM: Homo sapiens
       2513 <220> FEATURE:
       2515 <221> NAME/KEY: CDS
       2517 <222> LOCATION: (229)...(1857)
       2521 <400> SEQUENCE: 29
       2523 gttctcagat cggcttctcg caacaggcag tcagttctca ctgggcccct tggactccca         60
       2525 tttcaaaaat ggagaagaca gatcacagcc actgaccagg gaccgtggga ggtgccacgt        120
       2527 gatggtgagg catcatgcta gggagctgag ctctgacctt cctgctgggt gattctccac        180
       2529 ctctgggctg ctagatctac ttcctggatg ccgtgaagat cctcatgt atg aaa              234
       2531                                                           Met Lys
```

```
2533                                                             1
2535 atg aag tcc cag gca acc atg att tgc tgc tta gtg ttc ttt ctg tcc   282
2537 Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe Leu Ser
2539           5                   10                  15
2541 aca gaa tgt tcc cac tat aga tcc aag att cac cta aaa agc tat agt   330
2543 Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser Tyr Ser
2545          20                  25                  30
2547 gaa gtg gcc aac cac atc ctc gac aca gca gcc att tca aac tgg gct   378
2549 Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala
2551  35                  40                  45                  50
2553 ttc att ccc aac aaa aat gcc agc tcg gat ttg ttg cag tca gtg aat   426
2555 Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn
2557                  55                  60                  65
2559 ttg ttt gcc aga caa ctc cac atc cac aat aat tct gag aac att gtg   474
2561 Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val
2563          70                  75                  80
2565 aat gaa ctc ttc att cag aca aaa ggg ttt cac atc aac cat aat acc   522
2567 Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr
2569          85                  90                  95
2571 tca gag aaa agc ctc aat ttc tcc atg agc atg aac aat acc aca gaa   570
2573 Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu
2575         100                 105                 110
2577 gat atc tta gga atg gta cag att ccc agg caa gag cta agg aag ctg   618
2579 Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu
2581 115                 120                 125                 130
2583 tgg cca aat gca tcc caa gcc att agc ata gct ttc cca acc ttg ggg   666
2585 Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly
2587                 135                 140                 145
2589 gct atc ctg aga gaa gcc cac ttg caa aat gtg agt ctt ccc aga cag   714
2591 Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln
2593         150                 155                 160
2595 gta aat ggt ctg gtg cta tca gtg gtt tta cca gaa agg ttg caa gaa   762
2597 Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu
2599         165                 170                 175
2601 atc ata ctc acc ttc gaa aag atc aat aaa acc cgc aat gcc aga gcc   810
2603 Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala
2605         180                 185                 190
2607 cag tgt gtt ggc tgg cac tcc aag aaa agg aga tgg gat gag aaa gcg   858
2609 Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala
W--> 2611 195                 200                 205                 210
2613 tgc caa atg atg ttg gat atc agg aac gaa gtg aaa tgc cgc tgt aac   906
2615 Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn
W--> 2617                 215                 220                 225
2619 tac acc agt gtg gtg atg tct ttt tcc att ctc atg tcc tcc aaa tcg   954
2621 Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser
W--> 2623                 230                 235                 240
2625 atg acc gac aaa gtt ctg gac tac atc acc tgc att ggg ctc agc gtc   1002
2627 Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val
W--> 2629                 245                 250                 255
```

misc grid nos.

P.15

```
        2631 tca atc cta agc ttg gtt ctt tgc ctg atc att gaa gcc aca gtg tgg   1050
        2633 Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp
W--> 2635      260                 265                 270
        2637 tcc cgg gtg gtt gtg acg gag ata tca tac atg cgt cac gtg tgc atc   1098
        2639 Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val Cys Ile
W--> 2641 275                 280                 285                 290
        2643 gtg aat ata gca gtg tcc ctt ctg act gcc aat gtg tgg ttt atc ata   1146
        2645 Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe Ile Ile
W--> 2647                 295                 300                 305
        2649 ggc tct cac ttt aac att aag gcc cag gac tac aac atg tgt gtt gca   1194
        2651 Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys Val Ala
W--> 2653      310                 315                 320
        2655 gtg aca ttt ttc agc cac ttt ttc tac ctc tct ctg ttt ttc tgg atg   1242
        2657 Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe Trp Met
W--> 2659      325                 330                 335
        2661 ctc ttc aaa gca ttg ctc atc att tat gga ata ttg gtc att ttc cgt   1290
        2663 Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile Phe Arg
W--> 2665      340                 345                 350
        2667 agg atg atg aag tcc cga atg atg gtc att ggc ttt gcc att ggc tat   1338
        2669 Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile Gly Tyr
W--> 2671 355                 360                 365                 370
E--> 2673 ggg tgc cca ttg atc att gct gtc act aca gtt got atc aca gag cca   1386
        2675 Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro
W--> 2677                 375                 380                 385
        2679 gag aac ggc tac atg aga cct gag gcc tgt tgg ctt aac tgg gac aat   1434
        2681 Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn
W--> 2683      390                 395                 400
        2685 acc aaa gcc ctt tta gca ttt gcc atc ccg gcg ttc gtc att gtg gct   1482
        2687 Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala
W--> 2689      405                 410                 415
        2691 gta aat ctg att gtg gtt ttg gtt gtt gct gtc aac act cag agg ccc   1530
        2693 Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln Arg Pro
W--> 2695      420                 425                 430
        2697 tct att ggc agt tcc aag tct cag gat gtg gtc ata att atg agg atc   1578
        2699 Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile
W--> 2701 435                 440                 445                 450
        2703 agc aaa aat gtt gcc atc ctc act cca ctg ctg gga ctg acc tgg ggt   1626
        2705 Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly
W--> 2707                 455                 460                 465
        2709 ttt gga ata gcc act ctc ata gaa ggc act tcc ttg acg ttc cat ata   1674
        2711 Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile
W--> 2713      470                 475                 480
        2715 att ttt gcc ttg ctc aat gct ttc cag ggt ttt ttc atc ctg ctg ttt   1722
        2717 Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu Leu Phe
W--> 2719      485                 490                 495
        2721 gga acc att atg gat cac aag ata aga gat gct ttg agg atg agg atg   1770
        2723 Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met Arg Met
W--> 2725      500                 505                 510
        2727 tct tca ctg aag ggg aaa tcg agg gca gct gag aat gca tca cta ggc   1818
```

Misaligned nos.

invalid

```
     2729 Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser Leu Gly
W--> 2731 515                 520             525                 530
     2733 cca acc aat gga tct aaa tta atg aat cgt caa gga tgaaatgctg ccccat    1870
     2735 Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly
W--> 2737                 535             540
     2739 ttctcatgga tgtcctgaga ccaagagggg agatccagga gaaagaggcc atggaaagca    1930
     2741 ggctggagtg aggaggaatg gtcatgcttc cttggaagac tttctcttct tgtcaggagt    1990
     2743 gactcccaag ctcttggtcg gccgaagaaa aactgaggat aacatttgct gactgggctt    2050
     2745 taaggagcat gatttatgga cccttaacc tacccgtgcc ctgcaagagg ctggcttctt     2110
     2747 ggtcaatctt gactagatta agagtcaatc tgcaagccat tttatggtct ccctggccag    2170
     2749 ctgggggctg tagggccctg ctgggcttgg tcgtctttca ctcctgaggc ctgctctgtg    2230
     2751 gctccatagc tcagtcctcc atcactctgc gtggatcctg ggtactttgg acagtgaggg    2290
     2753 ttcgatccaa ttttagggggt aggggttgggg gtgggagtgg gagtgtgggt tggcaggagg   2350
     2755 aagaatgagt ctactttgga gacaattaag tcatggtacg tttcctaaag atagggaacg    2410
     2757 gaagaaaagc aagagaactg tttaatatgc tgattatttt agtctatttt agaccttgag    2470
     2759 taaactaatt tagcttctag gatccaagtt tccttatttg tgaaacagga aaaaaaaatt    2530
     2761 cttgtaggta ttactgtttg tgtgtttgag tttactgcac atgtttgtgt ttgtgtatat    2590
     2763 gtgtctttta aaaatactat atataaagaa gattctggtt gttatttttag acataaacga   2650
     2765 atatatgtac ctttcac                                                   2667
```

use letter "l" (lower-case), not numeral "1"

Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val

<400> 27

agcttccagc ccagtcggcc cggcccgggg gccatggagc tccgagcggc ggatcgcgag   60

cctcctgcga accccagcct gcacgcccgg ttagcattcg gccgggagat gcggcagtgg   120

aatctggaag ggcggtgaaa aacctacgtc ctgccctcgc ccggcctctc cattcgtccc   180

ccgggtagag aggtgcccgg ctcccacccc ttcccagccc cagccctgga gacagcagcc   240

cctagactac tgagggacag cgacagc atg aag gct ccg ggt cgg ctc gtg   291
                                Met Lys Ala Pro Gly Arg Leu Val
                                 1   5

ctc atc atc ctg tgc tcc gtg gtc ttc tct gcc gtc tac atc ctc ctg   339
Leu Ile Ile Leu Cys Ser Val Val Phe Ser Ala Val Tyr Ile Leu Leu
        10   15   20

tgc tgc tgg gcc ggc ctg ccc ctc tgc ctg gcc acc tgc ctg gac cac   387
Cys Cys Trp Ala Gly Leu Pro Leu Cys Leu Ala Thr Cys Leu Asp His
25   30   35   40

cac ttc ccc aca ggc tcc agg ccc act gtg ccg gga ccc ctg cac ttc   435
His Phe Pro Thr Gly Ser Arg Pro Thr Val Pro Gly Pro Leu His Phe
                    45   50   55

agt gga tat agc agt gtg cca gat ggg aag ccg ctg gtc cgc gag ccc   483
Ser Gly Tyr Ser Ser Val Pro Asp Gly Lys Pro Leu Val Arg Glu Pro

Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly Ser

do NOT use numeral 1 ! Use a lower-case "ℓ"

Input Set : **A:\01997.013000 sequence listing.txt**
Output Set: **N:\CRF4\04022003\J019114.raw**

```
L:20   M:270 C: Current Application Number differs, Replaced Current Application No
L:20   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:68   M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:129  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:199  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:300  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:374  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:492  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:562  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:719  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:885  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:1357 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1420 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1426 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1525 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1531 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1541 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1543 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1567 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1573 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:1817 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1823 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1829 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1841 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1853 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1855 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
```

Input Set : **A:\01997.013000 sequence listing.txt**
Output Set: **N:\CRF4\04022003\J019114.raw**

```
L:1859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1865 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1877 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1952 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2042 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2280 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2611 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2617 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2623 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2629 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2635 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2647 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2659 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2673 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2683 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2695 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2701 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2707 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2713 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:2885 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
```